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Serial No. 10/629,897

## IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with underlining and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please AMEND claims 1-3, 25, 26, 28 and 29 and ADD new claims 31 and 32 in accordance with the following:

1. (currently amended) A method for supporting a user in predicting a site where a target gene-expression sites on a genome is expressed, the site being one of a cell, a tissue and an organ, said method comprising:

calculating a first distance between the target gene and a first gene on the genome and a second distance between the target gene and a second genes gene on a the genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of known genes whose expression sites are known; and determining the expression sites of where the first gene based on the distance is smaller than the second distance;

extracting, from a database, a first site where the first gene is expressed and a second site where the second gene is expressed; and

outputting, as a list in which the first site is listed above the second site, a plurality of sites where the target gene is likely to be expressed.

2. (currently amended) The method according to claim 1, wherein ~~the calculating includes calculating both the first distance for each of the plurality of genes, and the determining includes determining the expression sites of the first gene as an expression site of at least one gene that has and the second distance are smaller than a predetermined distance relation among the plurality of genes threshold.~~

3. (currently amended) The method according to claim 1, wherein ~~the calculating includes calculating a first distance between the start position of the first gene and the is~~ between a start position of the target gene and a start position of the first gene, and the second distance is between the start position of the target gene and a start position of the second gene on the genome sequence.

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4. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the end position of the second gene on the genome sequence.

5. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and the end position of the second gene on the genome sequence.

6. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the start position of the second gene on the genome sequence.

7. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between first and second positions, the first position being between the start and end positions of the first gene on the genome sequence, and the second position being between the start and end positions of the second gene on the genome sequence.

8. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the start position of the second gene on the genome sequence.

9. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the end position of the second gene on the genome sequence.

10. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

11. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

12-24. (cancelled)

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25. (currently amended) A computer program product including computer executable instructions, ~~for predicting gene expression sites, supporting a user in predicting a site where a target gene on a genome is expressed, the site being one of a cell, a tissue and an organ, and wherein the instructions, when executed by the computer, cause the computer to perform a method comprising:~~

~~calculating a first distance between the target gene and a first gene on the genome and a second distance between the target gene and a second genes-gene on a the genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of genes whose expression sites are known; and determining the expression sites of where the first gene based on the distance is smaller than the second distance;~~

~~extracting, from a database, a first site where the first gene is expressed and a second site where the second gene is expressed; and~~

~~outputting, as a list in which the first site is listed above the second site, a plurality of sites where the target gene is likely to be expressed.~~

26. (currently amended) The computer program product according to claim 25, wherein ~~the determining include determining the expression sites of the first gene as an expression site of at least one gene that has both the first distance and the second distance are smaller than a predetermined distance relation among the plurality of genes threshold.~~

27. (cancelled)

28. (currently amended) An apparatus for supporting a user in predicting a site where a target gene expression on a genome is expressed, where the site is one of a cell, a tissue and an organ, said apparatus comprising:

a calculating unit that calculates a first distance between the target gene and a first gene on the genome and a second distance between the target gene and a second genes-gene on a the genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of genes whose expression sites are known; and a determination unit that determines the expression sites of where the first gene based on distance is smaller than the second distance;

an extracting unit that extracts, from a database, a first site where the first gene is expressed and a second site where the second gene is expressed; and

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an output unit that outputs, as a list in which the first site is listed above the second site, a plurality of sites where the target gene is likely to be expressed.

29. (currently amended) The apparatus according to claim 28, wherein ~~the calculation unit calculates the distance for each of the plurality of genes, and the determination unit determines the expression sites of the first gene as an expression site of at least one gene that~~ has both the first distance and the second distance are smaller than a predetermined distance relation among the plurality of genes threshold.

30. (cancelled)

31. (new) The method according to claim 1, wherein when the first site and the second site are identical, the second site is deleted from the list before being output.

32. (new) The method according to claim 2, wherein the predetermined threshold is determined based on a sensitivity and a specificity.